

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/899,422

DATE: 09/10/2001
TIME: 09:20:17

Input Set : A:\98385Hseq.txt
Output Set: N:\CRF3\09102001\I899422.raw

3 <110> APPLICANT: Hauptmann, Rudolph
4 Himmler, Adolph
5 Maurer-Fogy, Ingrid
6 Stratowa, Christian
8 <120> TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for
9 Them
11 <130> FILE REFERENCE: 98,385-H
13 <140> CURRENT APPLICATION NUMBER: 09/899,422
C--> 14 <141> CURRENT FILING DATE: 2001-08-21
16 <150> PRIOR APPLICATION NUMBER: 09/525,998
17 <151> PRIOR FILING DATE: 2000-03-15
19 <150> PRIOR APPLICATION NUMBER: 08/383,676
20 <151> PRIOR FILING DATE: 1995-02-01
22 <150> PRIOR APPLICATION NUMBER: 08/153,287
23 <151> PRIOR FILING DATE: 1993-11-17
25 <150> PRIOR APPLICATION NUMBER: 07/821,750
26 <151> PRIOR FILING DATE: 1992-01-02
28 <150> PRIOR APPLICATION NUMBER: 07/511,430
29 <151> PRIOR FILING DATE: 1990-04-20
31 <160> NUMBER OF SEQ ID NOS: 87
33 <170> SOFTWARE: PatentIn Ver. 2.0
35 <210> SEQ ID NO: 1
36 <211> LENGTH: 1368
37 <212> TYPE: DNA
38 <213> ORGANISM: Homo sapiens
40 <220> FEATURE:
41 <221> NAME/KEY: CDS
42 <222> LOCATION: (1)..(1368)
44 <220> FEATURE:
45 <221> NAME/KEY: sig_peptide
46 <222> LOCATION: (1)..(87)
48 <220> FEATURE:
49 <221> NAME/KEY: misc_feature
50 <222> LOCATION: (88)..(120)
51 <223> OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
52 extracellular proteases following secretion.
54 <220> FEATURE:
55 <221> NAME/KEY: misc_feature
56 <222> LOCATION: (606)..(633)
57 <223> OTHER INFORMATION: Portion of TNF-BP pro protein cleaved by
58 extracellular proteases following secretion.
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61 atg ggc ctc tcc acc gtg cct gac ctg ctg cca ctg gtg ctc ctg 48
62 Met Gly Leu Ser Thr Val Pro Asp Leu Leu Pro Leu Val Leu Leu
63 1 5 10 15
65 gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct 96
66 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro

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P. 5

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67	20	25	30	
69	cac cta ggg gac agg gag aag aga gat agt gtg tgt ccc caa gga aaa	144		
70	His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys			
71	35	40	45	
73	tat atc cac cct caa aat aat tcg att tgc tgt acc aag tgc cac aaa	192		
74	Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys			
75	50	55	60	
77	gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac	240		
78	Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp			
79	65	70	75	80
81	tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc	288		
82	Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu			
83	85	90	95	
85	aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg	336		
86	Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val			
87	100	105	110	
89	gag atc tct tct tgc aca gtg gac ccg gac acc gtg tgt ggc tgc agg	384		
90	Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg			
91	115	120	125	
93	aag aac cag tac ccg cat tat tgg agt gaa aac ctt ttc cag tgc ttc	432		
94	Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe			
95	130	135	140	
97	aat tgc agc ctc tgc aat ggg acc gtg cac ctc tcc tgc cag gag	480		
98	Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu			
99	145	150	155	160
101	aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttt cta aga gaa	528		
102	Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu			
103	165	170	175	
105	aac gag tgt tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg	576		
106	Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Ser Leu Glu Cys Thr			
107	180	185	190	
109	aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca	624		
110	Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser			
111	195	200	205	
113	ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt	672		
114	Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu			
115	210	215	220	
117	tta tcc ctc ctc att ggt tta atg tat cgc tac caa ccg tgg aag	720		
118	Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys			
119	225	230	235	240
121	tcc aag ctc tac tcc att gtt tgt ggg aaa tcg aca cct gaa aaa gag	768		
122	Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu			
123	245	250	255	
125	ggg gag ctt gaa gga act act aat aag ccc ctg gcc cca aac cca agc	816		
126	Gly Glu Leu Glu Gly Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser			
127	260	265	270	
129	ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg	864		
130	Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val			
131	275	280	285	

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133	ccc	agt	tcc	acc	ttc	acc	tcc	agc	tcc	acc	tat	acc	ccc	ggt	gac	tgt	912
134	Pro	Ser	Ser	Thr	Phe	Thr	Ser	Ser	Ser	Thr	Tyr	Thr	Pro	Gly	Asp	Cys	
135																300	
136	290				295												
137	ccc	aac	ttt	gct	ccc	cgc	aga	gag	gtg	gca	cca	ccc	tat	cag	ggg	960	
138	Pro	Asn	Phe	Ala	Ala	Pro	Arg	Arg	Glu	Val	Ala	Pro	Pro	Tyr	Gln	Gly	
139	305				310						315					320	
140	gct	gac	ccc	atc	ctt	gct	aca	gcc	ctc	gcc	tcc	gac	ccc	atc	ccc	aac	1008
141	Ala	Asp	Pro	Ile	Leu	Ala	Thr	Ala	Leu	Ala	Ser	Asp	Pro	Ile	Pro	Asn	
142																	
143	325				330											335	
144	ccc	ctt	cag	aag	tgg	gag	gac	gac	gcc	cac	aag	cca	cag	agc	cta	gac	1056
145	Pro	Leu	Gln	Lys	Trp	Glu	Asp	Ser	Ala	His	Lys	Pro	Gln	Ser	Leu	Asp	
146																	
147	340				345											350	
148	act	gat	gac	ccc	gct	acg	ctg	tac	gcc	gtg	gtg	gag	aac	gtg	ccc	ccg	1104
149	Thr	Asp	Asp	Pro	Ala	Thr	Leu	Tyr	Ala	Val	Val	Glu	Asn	Val	Val	Pro	
150																	
151	355				360											365	
152	ttg	cgc	tgg	aag	gaa	ttc	gtg	cgg	cgc	cta	ggg	ctg	agc	gac	cac	gag	1152
153	Leu	Arg	Trp	Lys	Glu	Phe	Val	Arg	Arg	Leu	Gly	Leu	Ser	Asp	His	Glu	
154																	
155	370				375											380	
156	atc	gat	cgg	ctg	gag	ctg	cag	aac	ggg	cgc	tgc	ctg	cgc	gag	gct	caa	1200
157	Ile	Asp	Arg	Leu	Glu	Leu	Gln	Asn	Gly	Arg	Cys	Leu	Arg	Glu	Ala	Gln	
158																	
159	385				390						395					400	
160	tac	agc	atg	ctg	gct	acc	tgg	agg	cgg	cgc	acg	ccg	cgg	cgc	gag	gcc	1248
161	Tyr	Ser	Met	Leu	Ala	Thr	Trp	Arg	Arg	Arg	Arg	Thr	Pro	Arg	Arg	Glu	
162																	
163	405				410											415	
164	acg	ctg	gag	ctg	ctg	gga	cgc	gtg	ctc	cgc	gac	atg	gac	ctg	ctg	ggc	1296
165	Thr	Leu	Glu	Leu	Gly	Arg	Val	Leu	Arg	Asp	Met	Asp	Leu	Leu	Gly		
166																	
167	420				425											430	
168	tgc	ctg	gag	atc	gag	gag	gct	ttt	tgc	ggc	ccc	gcc	gcc	ctc	ccg		1344
169	Cys	Leu	Glu	Asp	Ile	Glu	Ala	Leu	Cys	Gly	Pro	Ala	Ala	Leu	Pro		
170																	
171	435				440											445	
172	ccc	gct	ccc	agt	ctt	ctc	aga	tga									1368
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177	<211>	LENGTH:	455														
178	<212>	TYPE:	PRT														
179	<213>	ORGANISM:	Homo sapiens														
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182	1		5			10										15	
183	Glu	Leu	Leu	Val	Gly	Ile	Tyr	Pro	Ser	Gly	Val	Ile	Gly	Leu	Val	Pro	
184																	
185	20		25			30											
186	His	Leu	Gly	Asp	Arg	Glu	Lys	Arg	Asp	Ser	Val	Cys	Pro	Gln	Gly	Lys	
187	35		40			45											
188	Tyr	Ile	His	Pro	Gln	Asn	Asn	Ser	Ile	Cys	Cys	Thr	Lys	Cys	His	Lys	
189	50		55			60											
190	Gly	Thr	Tyr	Leu	Tyr	Asn	Asp	Cys	Pro	Gly	Pro	Gly	Gln	Asp	Thr	Asp	
191	65		70			75										80	
192	Cys	Arg	Glu	Cys	Glu	Ser	Gly	Ser	Phe	Thr	Ala	Ser	Glu	Asn	His	Leu	

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200	85	90	95	
202	Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val			
203	100	105	110	
205	Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg			
206	115	120	125	
208	Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe			
209	130	135	140	
211	Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu			
212	145	150	155	160
214	Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu			
215	165	170	175	
217	Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr			
218	180	185	190	
220	Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser			
221	195	200	205	
223	Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu			
224	210	215	220	
226	Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys			
227	225	230	235	240
229	Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu			
230	245	250	255	
232	Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser			
233	260	265	270	
235	Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val			
236	275	280	285	
238	Pro Ser Ser Thr Phe Thr Ser Ser Thr Tyr Thr Pro Gly Asp Cys			
239	290	295	300	
241	Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly			
242	305	310	315	320
244	Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn			
245	325	330	335	
247	Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp			
248	340	345	350	
250	Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro			
251	355	360	365	
253	Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu			
254	370	375	380	
256	Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln			
257	385	390	395	400
259	Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala			
260	405	410	415	
262	Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly			
263	420	425	430	
265	Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro			
266	435	440	445	
268	Pro Ala Pro Ser Leu Leu Arg			
269	450	455		
272	<210> SEQ ID NO: 3			
273	<211> LENGTH: 483			

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274 <212> TYPE: DNA
275 <213> ORGANISM: Homo sapiens
277 <220> FEATURE:
278 <221> NAME/KEY: CDS
279 <222> LOCATION: (1)..(483)
281 <400> SEQUENCE: 3
282 gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat tcg 48
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284 1 5 10 15
286 att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt 96
287 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
288 20 25 30
290 cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc 144
291 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
292 35 40 45
294 ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa 192
295 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
296 50 55 60
298 tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac 240
299 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
300 65 70 75 80
302 cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg 288
303 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
304 85 90 95
306 agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg 336
307 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
308 100 105 110
310 acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc 384
311 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
312 115 120 125
314 cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac 432
315 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
316 130 135 140
318 tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag 480
319 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
320 145 150 155 160
322 aat 483
323 Asn
326 <210> SEQ ID NO: 4
327 <211> LENGTH: 161
328 <212> TYPE: PRT
329 <213> ORGANISM: Homo sapiens
331 <400> SEQUENCE: 4
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333 1 5 10 15
335 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
336 20 25 30
338 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
339 35 40 45

VERIFICATION SUMMARY
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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:815 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:847 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:1439 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19
L:1485 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1626 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1670 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:1689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:1692 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34
L:1725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36